What is claimed:

1. An isolated nucleic acid molecule from *Corynebacterium glutamicum* encoding a metabolic pathway protein selected from the group consisting of a nucleic acid molecule comprising the nucleotide sequence set forth in SEQ ID NO:1, SEQ ID NO:3, or SEQ ID NO:5.

2. The isolated nucleic acid molecule of claim 1, wherein said metabolic pathway protein is involved in the metabolism of an amino acid.

3. An isolated nucleic acid molecule which encodes a naturally occurring allelic variant of a polypeptide selected from the group of amino acid sequences consisting of those sequences set forth in SEQ ID NO:2, SEQ ID NO:4, or SEQ ID NO:6.

4. An isolated nucleic acid molecule comprising a nucleotide sequence which is at least 50% homologous to a nucleotide sequence set forth in SEQ ID NO:6, or a complement thereof.

5. An isolated nucleic acid molecule comprising a nucleotide sequence which is at least 65% homologous to a nucleotide sequence set forth in SEQ ID NO:1, or a complement thereof.

6. An isolated nucleic acid molecule comprising a fragment of at least 15 nucleotides of a nucleic acid comprising a nucleotide sequence selected from the group consisting of those sequences set forth set forth in SEQ ID NO:1, SEQ ID NO:3, or SEQ ID NO:5.

7. An isolated nucleic acid molecule which hybridizes to the nucleic acid molecule of any one of claims 1-6 under stringent conditions.

8. An isolated nucleic acid molecule comprising the nucleic acid molecule of claim 1, or a portion thereof, and a nucleotide sequence encoding a heterologous polypeptide.

9. A vector comprising the nucleic acid molecule of claim 1.

10. The vector of claim 9, further comprising one or more metabolic pathway nucleic acid molecules.

11. The vector of claim 9 or 10, which is an expression vector.

12. A host cell transfected with the expression vector of claim 9 or 10.

13. The vector of claim 10, wherein the second metabolic pathway nucleic acid molecule is selected from the group consisting of a nucleic acid molecule comprising the nucleotide sequence set forth in the odd-numbered sequences listed in Table 1, excluding any F-designated nucleic acid molecules.

14. The host cell of claim 12, wherein said cell is a microorganism.

15. The host cell of claim 12, wherein said cell belongs to the genus *Corynebacterium* or *Brevibacterium*.

16. The host cell of claim 12, wherein the expression of said nucleic acid molecules results in the modulation in production of a fine chemical from said cell.

17. The host cell of claim 16, wherein said fine chemical is an amino acid.

18. The host cell of claim 17, wherein said amino acid is methionine or lysine.

19. A method of producing a polypeptide comprising culturing the host cell of claim 12 in an appropriate culture medium to, thereby, produce the polypeptide.

20. An isolated metabolic pathway polypeptide from *Corynebacterium glutamicum*, or a portion thereof.

21. The protein of claim 20, wherein said polypeptide is selected from the group of metabolic pathway proteins which participate in the metabolism of an amino acid.

22. The protein of claim 21, wherein said amino acid is methionine or lysine.

23. An isolated nucleic acid molecule from *Corynebacterium glutamicum* which encodes a metabolic pathway protein comprising the amino acid sequence set forth in SEQ ID NO:2, SEQ ID NO:4, or SEQ ID NO:6.

24. An isolated polypeptide comprising a naturally occurring allelic variant of a polypeptide comprising an amino acid sequence selected from the group consisting of those sequences set forth in SEQ ID NO:2, SEQ ID NO:4, or SEQ ID NO:6.

25. The isolated polypeptide of claim 23, further comprising heterologous amino acid sequences.

26. An isolated polypeptide comprising a nucleotide sequence which is at least 50% homologous to a nucleotide sequence set forth in SEQ ID NO:5, or a complement thereof.

27. An isolated polypeptide comprising a nucleotide sequence which is at least 65% homologous to a nucleotide sequence set forth in SEQ ID NO:1, or a complement thereof.

28. A method for producing a fine chemical, comprising culturing a cell containing a vector of claim 9 or 10, such that the fine chemical is produced.

29. The method of claim 28, wherein said cell is cultured in the presence of a sulfur source.

30. The method of claim 28, wherein said method further comprises the step of recovering the fine chemical from said culture.

31. The method of claim 28, wherein said fine chemical is an amino acid.

32. The method of claim 31, wherein said amino acid is methionine or lysine.

33. The method of claim 28, wherein said method further comprises the step of transfecting said cell with the vector of claim 9 or 10, to result in a cell containing said vector.

34. The method of claim 28, wherein said cell belongs to the genus *Corynebacterium* or *Brevibacterium*.

35. The method of claim 27, wherein said cell is selected from the group consisting of: *Corynebacterium glutamicum, Corynebacterium herculis, Corynebacterium, lilium, Corynebacterium acetoacidophilum, Corynebacterium acetoglutamicum, Corynebacterium acetophilum, Corynebacterium ammoniagenes, Corynebacterium fujiokense, Corynebacterium nitrilophilus, Brevibacterium ammoniagenes, Brevibacterium butanicum, Brevibacterium divaricatum, Brevibacterium flavum, Brevibacterium healii, Brevibacterium ketoglutamicum, Brevibacterium ketosoreductum, Brevibacterium lactofermentum, Brevibacterium linens, Brevibacterium paraffinolyticum,* and those strains set forth in Table 3.

36. A method for producing a fine chemical, comprising culturing a cell whose genomic DNA has been altered by the inclusion of a nucleic acid molecule of any one of claims 1-6.

37. A method for producing a fine chemical, comprising culturing a cell whose genomic DNA has been altered by the inclusion of a nucleic acid molecule of any one of claims 1-6, alone or in combination with another metabolic pathway nucleic acid selected from the group consisting of a nucleic acid molecule comprising the nucleotide sequence set forth in the odd-numbered sequences listed in Table 1, excluding any F-designated nucleic acid molecules.

38. A method for producing a fine chemical, comprising culturing a cell whose genomic DNA has been altered by the inclusion of a nucleic acid molecule of any one of claims 1-6, alone or in combination with one or more metabolic pathway nucleic acid molecule.

39. The method of claim 36, wherein the metabolic pathway nucleic acid molecule is selected from the group consisting of *metZ, metC, metB, metA, metE, metH, hom, asd, lysC, lysC/ask,* rxa00657, *dapA, dapB, dapC, dapD/argD, dapE, dapF, lysA, ddh, lysE, lysG, lysR, hsk, ppc, pycA, accD, accA, accB, accC, gpdh* genes encoding glucose-6-phophate-dehydrogenase, *opcA, pgdh, ta, tk, pgl, rlpe, rpe* or any combination of the above-mentioned genes.

40. The method of claim 35 or 36, wherein said metabolic pathway is methionine or lysine metabolism.

41. A method of modulating the yield of a fine chemical from a cell comprising, introducing one or more metabolic pathway genes into a cell, thereby modulating the yield of a fine chemical.

42. The method of claim 41, wherein said metabolic pathway gene or genes are integrated into the chromosome of the cell.

43. The method of claim 41, wherein said metabolic pathway gene or genes are maintained on a plasmid.

44. The method of claim 41, wherein said fine chemical is an amino acid.

45. The method of claim 44, wherein said amino acid is methionine or lysine.

46. The method of claim 41, wherein said metabolic pathway gene or genes are selected from the group consisting of the nucleic acid molecule of any one of claims 1-6.

47. The method of claim 41, wherein the nucleotide sequence of said metabolic pathway gene or genes has been mutated to increase yield of a fine chemical.